

## SEQUENCE LISTING

<110> Kere, Juha  
 Taipale, Mikko  
 Nopola-Hemmi, Jaana  
 Kaminen, Nina

<120> Novel Human Gene Functionally Related To Dyslexia

<130> DYXC1

<140>

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1263

<212> DNA

<213> Homo sapiens

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<223> coding sequence for human DYXC1 (cDNA)

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<222> (369)..(1628)

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<223> human DYXC1 mRNA as cDNA

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Thr Ala Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp
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Thr Asp Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro
             35             40             45

ttt tta ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc 554
Phe Leu Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser
             50             55             60

aaa gca aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa 602
Lys Ala Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys
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Glu Ala Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu
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atg atg caa aga att aga gaa aaa tct att tta caa gca caa gag aga 698
Met Met Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg
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aaa ata gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gca 842
Lys Ile Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Ala
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Leu Glu Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys
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Arg Asn Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu	210	215	220	
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Lys Leu Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile	225	230	235	
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Lys Ile Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser	240	245	250	
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Gln Val Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg	255	260	265	270
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Thr Glu Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg	305	310	315	
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Leu Lys Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala	335	340	345	350
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Leu Glu Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met	355	360	365	
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Lys Ala His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr	370	375	380	
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Val Glu Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser	385	390	395	
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Asn Lys Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln	400	405	410	
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<212> PRT

<213> Homo sapiens

<223> human DYXC1 mRNA as cDNA

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Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Gly	Arg
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210	215	220
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Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala		
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Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys		
	275	280 285
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu		
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Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn		
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Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys		
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Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu		
	340	345 350
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala		
	355	360 365
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu		
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Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys		
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Ser	Leu	Pro	Leu	Arg	Gly	Val	Cys	Val	Arg	Asp	Ala	Asp	Val	Phe	Cys	
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Gly	Glu	Ser	Tyr	Leu	Lys	Val	Asn	Phe	Pro	Pro	Phe	Leu	Phe	Glu	Leu	
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Phe	Leu	Tyr	Ala	Pro	Ile	Asp	Asp	Gly	Lys	Ser	Lys	Ala	Lys	Ile	Gly	
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Asn	Asp	Thr	Ile	Leu	Phe	Thr	Leu	Tyr	Lys	Lys	Glu	Pro	Val	Leu	Trp	
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Asp	Ser	Leu	Ser	Val	Pro	Gly	Val	Asp	Lys	Glu	Met	Met	Gln	Arg	Ile	
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Glu	Ala	Lys	Ala	Val	Ala	Lys	Arg	Glu	Asp	Gln	Arg	Tyr	Ala	Leu	Gly	
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gag	atg	atg	aag	att	gaa	gaa	gaa	gag	agg	aaa	aaa	ctc	gaa	gat	ctg	488
Glu	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Leu	Glu	Asp	Leu	
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Arg	Asn	Trp	Glu	Asn	Ile	Phe	Pro	Glu	Lys	Leu	Lys	Glu	Asp	Arg	Val	
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Pro	Ala	Pro	Arg	Ser	Ala	Gly	Ser	Ile	Gln	Ile	Ser	Phe	Thr	Pro	Arg	
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gtg	ttc	cca	aca	gca	ctt	cgg	gaa	tcc	caa	gtc	gca	gaa	gag	gag	gag	824
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Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala Met Ser Thr Asp Leu			
260	265	270	275
cct gag ttc ttt gac tta aaa gaa gaa gag agg aat cca gac tgg ttg			920
Pro Glu Phe Phe Asp Leu Lys Glu Glu Glu Arg Asn Pro Asp Trp Leu			
	280	285	290
aaa gac aag gga aac aaa ttg ttt gca aca gaa aac tat ttg gca gcg			968
Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu Asn Tyr Leu Ala Ala			
	295	300	305
gtt gat gca tat aat tta gcc ata cga ctg aac tgt aag atc cca tta			1016
Val Asp Ala Tyr Asn Leu Ala Ile Arg Leu Asn Cys Lys Ile Pro Leu			
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	325	330	335
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	340	345	350
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Val Ala Asp Asn Ala Asn Ala Arg Met Lys Ala His Val Arg Arg Gly			
	360	365	370
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Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu Gly Leu Gln Asp Tyr			
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Glu Ala Ala Leu Lys Ile Asp Pro Ala Asn Thr Val Val Gln Asn Asp			
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Ala Glu Lys Ile Arg Asn Ile Ile Gln Gly Thr Ala Leu Lys Ser Arg			
	405	410	415
gac tagaggcagc taggcacagg agtctctgca agtactgtag ctctgtacag			1357
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420			
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&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;223&gt; murine DYXC1 mRNA as cDNA

&lt;400&gt; 5

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Val	Phe	Cys	Gly	Glu	Ser	Tyr	Leu	Lys	Val	Asn	Phe	Pro	Pro	Phe	Leu
		35					40					45			
Phe	Glu	Leu	Phe	Leu	Tyr	Ala	Pro	Ile	Asp	Asp	Gly	Lys	Ser	Lys	Ala
	50					55					60				
Lys	Ile	Gly	Asn	Asp	Thr	Ile	Leu	Phe	Thr	Leu	Tyr	Lys	Lys	Glu	Pro
65					70					75					80
Val	Leu	Trp	Asp	Ser	Leu	Ser	Val	Pro	Gly	Val	Asp	Lys	Glu	Met	Met
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Gln	Arg	Ile	Arg	Glu	Lys	Ser	Ile	Leu	Gln	Ala	Gln	Glu	Lys	Ala	Lys
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	290					295					300				



Leu Ala Ala Val Asp Ala Tyr Asn Leu Ala Ile Arg Leu Asn Cys Lys  
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 325 330 335  
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 340 345 350  
 Thr Pro Pro Val Ala Asp Asn Ala Asn Ala Arg Met Lys Ala His Val  
 355 360 365  
 Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu Gly Leu  
 370 375 380  
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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: RT-PCR primer

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<210> 12  
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<223> Description of Artificial Sequence: RT-PCR primer

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gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac acg gac 96  
Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp  
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gtg ttc tgc atg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta 144  
Val Phe Cys Met Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu  
35 40 45

ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca 192  
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
50 55 60

aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg 240  
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
65 70 75 80

gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg 288  
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met  
85 90 95

caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa 336  
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
100 105 110

gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat 384  
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr  
115 120 125

gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa aaa ata 432  
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130 135 140

gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa	480
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu	
145 150 155 160	
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Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln	
165 170 175	
aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa gaa aga	576
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	
180 185 190	
aaa aaa ata aaa tat aag agt ctt act aga aat ttg gca tct aga aat	624
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	
195 200 205	
ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta	672
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	
210 215 220	
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Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile	
225 230 235 240	
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta	768
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	
245 250 255	
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca	816
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	
260 265 270	
atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa gaa aag	864
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	
275 280 285	
aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa	912
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	
290 295 300	
aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat	960
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn	
305 310 315 320	
aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa	1008
Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys	
325 330 335	
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa	1056
Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu	
340 345 350	
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca	1104
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
355 360 365	
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa	1152
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	

ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa 1200  
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 385 390 395 400

att gta caa att gat gct gag aag att cgg aat gta att caa gga aca 1248  
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 Glu Leu Lys Ser  
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<213> Pan troglodytes

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 35 40 45

Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
 50 55 60

Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
 65 70 75 80

Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met  
 85 90 95

Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
 100 105 110

Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr  
 115 120 125

Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile  
 130 135 140

Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu  
 145 150 155 160

Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln  
 165 170 175

Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg  
 180 185 190

Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn  
 195 200 205

Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu  
 210 215 220

Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile  
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 Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala  
 260 265 270  
 Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys  
 275 280 285  
 Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu  
 290 295 300  
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn  
 305 310 315 320  
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys  
 325 330 335  
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 340 345 350  
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala  
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 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu  
 370 375 380  
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys  
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 Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp  
 20 25 30  
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Phe	Glu	Ala	Phe	Leu	Tyr	Ala	Pro	Ile	Asp	Asp	Glu	Ser	Ser	Lys	Ala	
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aag	att	ggg	aat	gac	acc	att	gtc	ttc	acc	ttg	tat	aaa	aaa	gaa	gcg	240
Lys	Ile	Gly	Asn	Asp	Thr	Ile	Val	Phe	Thr	Leu	Tyr	Lys	Lys	Glu	Ala	
65					70					75					80	
gcc	atg	tgg	gag	acc	ctt	tct	gtg	acg	ggg	ggt	gac	aaa	gag	atg	atg	288
Ala	Met	Trp	Glu	Thr	Leu	Ser	Val	Thr	Gly	Val	Asp	Lys	Glu	Met	Met	
85					90					95						
caa	aga	att	aga	gaa	aaa	tct	att	tta	caa	gca	caa	gag	aga	gca	aaa	336
Gln	Arg	Ile	Arg	Glu	Lys	Ser	Ile	Leu	Gln	Ala	Gln	Glu	Arg	Ala	Lys	
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Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr	
115					120					125						
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Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile	
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Ala	Trp	Lys	Glu	Tyr	Gln	Arg	Lys	Ala	Glu	Glu	Gln	Lys	Glu	Ile	Gln	
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Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg	
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195					200					205						
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Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile	
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Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val	
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Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala	
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Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys	
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aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat 960  
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aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa 1008  
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 370 375 380

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 385 390 395 400

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 Glu Leu Lys Ser  
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Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
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Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
 65 70 75 80

Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met  
 85 90 95



Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
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 Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu  
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 Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg  
 180 185 190  
 Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn  
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 210 215 220  
 Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile  
 225 230 235 240  
 Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val  
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 275 280 285  
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 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn  
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 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu  
 370 375 380  
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys  
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gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac acg gac 96  
Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp  
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gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta 144  
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu  
35 40 45

ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca 192  
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
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aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg 240  
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
65 70 75 80

gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag acg atg 288  
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met  
85 90 95

caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa 336  
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys  
100 105 110

gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat 384  
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr  
115 120 125

gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa aaa ata 432  
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile  
130 135 140

gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa 480  
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145 150 155 160

gcc tgg aaa gaa tat caa aga aaa gct gag gag cac aaa aaa att cag 528  
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu His Lys Lys Ile Gln  
165 170 175

aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa gaa aga 576  
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180	185	190	
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ctt gct cca aaa gga aga aat tca gaa aat ata ttt act gag aag tta Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu 210 215 220			672
aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile 225 230 235 240			720
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val 245 250 255			768
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala 260 265 270			816
atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa gaa aag Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys 275 280 285			864
aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu 290 295 300			912
aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn 305 310 315 320			960
aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys 325 330 335			1008
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu 340 345 350			1056
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala 355 360 365			1104
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370 375 380			1152
ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys 385 390 395 400			1200
att gta caa att gat gct gag aag att cgg aat gta att caa gga aca Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr 405 410 415			1248
gaa cta aaa tct taa Glu Leu Lys Ser 420			1263

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Val	Phe	Cys	Thr	Glu	Asn	Tyr	Leu	Lys	Val	Asn	Phe	Pro	Pro	Phe	Leu
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Phe	Glu	Ala	Phe	Leu	Tyr	Ala	Pro	Ile	Asp	Asp	Glu	Ser	Ser	Lys	Ala
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Ala	Met	Trp	Glu	Thr	Leu	Ser	Val	Thr	Gly	Val	Asp	Lys	Glu	Thr	Met
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Gln	Arg	Ile	Arg	Glu	Lys	Ser	Ile	Leu	Gln	Ala	Gln	Glu	Arg	Ala	Lys
			100					105					110		
Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr
		115					120					125			
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile
	130					135					140				
Glu	Asp	Met	Lys	Glu	Asn	Glu	Arg	Ile	Lys	Ala	Thr	Lys	Glu	Leu	Glu
145					150					155					160
Ala	Trp	Lys	Glu	Tyr	Gln	Arg	Lys	Ala	Glu	Glu	His	Lys	Lys	Ile	Gln
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Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg
			180					185					190		
Lys	Lys	Leu	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Ser	Ala	Ser	Arg	Asn
		195					200					205			
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu
	210					215					220				
Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile
225					230					235					240
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val
				245					250					255	
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala
			260					265					270		
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys
		275					280					285			

Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu  
 290 295 300  
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn  
 305 310 315 320  
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys  
 325 330 335  
 Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu  
 340 345 350  
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala  
 355 360 365  
 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu  
 370 375 380  
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys  
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 Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr  
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 Glu Leu Lys Ser  
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 gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac acg gac 96  
 Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp  
 20 25 30  
 gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta 144  
 Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu  
 35 40 45  
 ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca 192  
 Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala  
 50 55 60  
 aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg 240  
 Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala  
 65 70 75 80  
 gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg 288

Ala	Met	Trp	Glu	Thr	Leu	Ser	Val	Thr	Gly	Val	Asp	Lys	Glu	Met	Met	
				85					90					95		
caa	aga	att	aga	gaa	aaa	tct	att	tta	caa	gca	caa	gag	aga	gca	aaa	336
Gln	Arg	Ile	Arg	Glu	Lys	Ser	Ile	Leu	Gln	Ala	Gln	Glu	Arg	Ala	Lys	
			100					105					110			
gaa	gct	aca	gaa	gca	aaa	gct	gca	gca	aag	cgg	gaa	gat	caa	aaa	tat	384
Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr	
		115					120					125				
gca	cta	agt	gtc	atg	atg	aag	att	gaa	gaa	gaa	gag	agg	aaa	aaa	ata	432
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile	
	130					135						140				
gaa	gat	atg	aaa	gaa	aat	gaa	cgg	ata	aaa	gcc	act	aaa	gaa	ttg	gaa	480
Glu	Asp	Met	Lys	Glu	Asn	Glu	Arg	Ile	Lys	Ala	Thr	Lys	Glu	Leu	Glu	
145					150					155					160	
gcc	tgg	aaa	gaa	tat	caa	aga	aaa	gct	gag	gag	caa	aaa	aaa	att	cag	528
Ala	Trp	Lys	Glu	Tyr	Gln	Arg	Lys	Ala	Glu	Glu	Gln	Lys	Lys	Ile	Gln	
				165					170					175		
aga	gaa	gag	aaa	tta	tgt	caa	aaa	gaa	aag	caa	att	aaa	gaa	gaa	aga	576
Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg	
			180					185					190			
aaa	aaa	ata	aaa	tat	aag	agt	ctt	act	aga	aat	ttg	gca	tct	aga	aat	624
Lys	Lys	Ile	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Leu	Ala	Ser	Arg	Asn	
		195					200					205				
ctt	gct	cca	aaa	ggg	aga	aat	tca	gaa	aat	ata	ttt	act	gag	aag	tta	672
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu	
	210					215					220					
aag	gaa	gac	agt	att	cct	gct	cct	cgc	tct	gtt	ggc	agt	att	aaa	atc	720
Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile	
225					230					235					240	
aac	ttt	acc	cct	cga	gta	ttc	cca	aca	gct	ctt	cgt	gaa	tca	caa	gta	768
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val	
				245					250					255		
gca	gaa	gag	gag	gag	tgg	ctg	cac	aaa	caa	gct	gag	gca	cga	aga	gca	816
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala	
			260					265					270			
atg	aat	act	gac	ata	gct	gaa	ctt	tgc	gat	tta	aaa	gaa	gaa	gaa	aag	864
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys	
		275					280					285				
aac	cca	gaa	tgg	ttg	aag	gat	aaa	gga	aac	aaa	ttg	ttt	gca	aca	gaa	912
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu	
	290					295					300					
aac	tat	ttg	gca	gct	atc	aat	gca	tat	aat	tta	gcc	ata	aga	cta	aat	960
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn	
305					310					315					320	
aat	aag	atg	cca	cta	ttg	tat	ttg	aac	cgg	gct	gct	tgc	cac	cta	aaa	1008
Asn	Lys	Met	Pro	Leu	Leu	Tyr	Leu	Asn	Arg	Ala	Ala	Cys	His	Leu	Lys	

325	330	335	
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu 340 345 350			1056
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala 355 360 365			1104
cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370 375 380			1152
ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys 385 390 395 400			1200
att gta caa att gat gct gag aag att cgg aat gta att caa gga aca Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr 405 410 415			1248
gaa cta aaa tct taa Glu Leu Lys Ser 420			1263

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&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Pan paniscus

&lt;400&gt; 20

Met Pro Leu Gln Val Ser Asp Tyr Ser Trp Gln Gln Thr Lys Thr Ala 1 5 10 15
Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp 20 25 30
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu 35 40 45
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala 50 55 60
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala 65 70 75 80
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met 85 90 95
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys 100 105 110
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr 115 120 125
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile 130 135 140
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu



145		150		155		160
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln						
		165		170		175
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg						
		180		185		190
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn						
		195		200		205
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu						
		210		215		220
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile						
		225		230		240
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val						
		245		250		255
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala						
		260		265		270
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys						
		275		280		285
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu						
		290		295		300
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn						
		305		310		315
Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys						
		325		330		335
Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu						
		340		345		350
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala						
		355		360		365
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu						
		370		375		380
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys						
		385		390		395
Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr						
		405		410		415
Glu Leu Lys Ser						
		420				

&lt;210&gt; 21

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

Cys Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys

1

5

10

15